

feline (from cDNA) YEIAPVFVILMEQITLKKMREIIVGSSKDGDGIFSPGGAIISNMYSIMAAARYKFFPEVKTKG

rat (from peptide) YEIAPVFVILLEYV - - - REIIIGWPGGS - DGIFSPGGAIISN - YAMLIARYKMFPEVKEKG

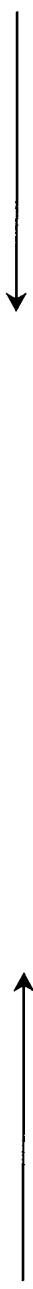
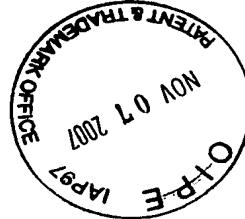


Figure 1



GGGCGTGGGGCTCGAGGCCAAGCAGCTTGGCCCACTCGGAGGGACCGGCCA
 10
 M A S P G S G F W S F G S E D G
 GACTAGCAGAACCCATGGCATCTCCGGCTCTGGCTTTGGATCTGGATCTGAAGATG
 70
 S G D P E N P G T A R A W C Q V A Q K F
 GCTCTGGGATCCTGAGAACCCGGAAACAGCGAGAGCCAGGGAGACTCTGAGAAGCCAG
 130
 T G G I G N K L C A L L Y G D S E K P A
 TCACGGGGCATCGGAAACAAAGCTATCGGCTCTGCTCTACGGAGACTCTGAGAAGCCAG
 190
 E S G G S V T S R A A T R K V A C T C D
 210
 CAGAGAGGGAGGGACTCGGGCCAAAGGAGATGTCAATTATGCACCTCTCCACGCCAG
 250
 Q K P C S C P K G D V N Y A L L H A T D
 ACCAAAAACCCCTGCAGCTGGCCCAAGGAGATGTCAATTATGCACCTCTCCACGCCAG
 270
 290
 L L P A C E G E R P T L A F L Q D V M N
 ACCTGGCTGCCAGGCCACTCGGCAAGGAGAAAGGCCACTCTGGCATTCTGCAAGATGTAATGA
 310
 330
 350
 370
 390
 410
 I L L Q Y V V K S F D R S T K V I D F H
 ACATTTGCTTCAGTACGTGGAAAAGTTTGATAGATCAACTAAAGTGATTGATTCC
 430
 450
 470
 Y P N E L L Q E Y N W E L A D Q P Q N L
 ATTACCCCAATGAGCTTCAAGAGTATAATTGGAAATTGGCAGACCCAACCGCAAAATC
 490
 510
 530
 E E I L T H C Q T T L K Y A I K T G H P

Figure 2A

TGGAGGAAATTGACGGCACTGCCAAACAACTCTAAATATGCCATTAAACAGGGCATC
 550
 R Y F N Q L S T G L D M V G L A A D W L
 CCCGATATTAAATCAGCTGTCTACCGGATTGGATATGGTTGGATTAGCAGGATTGGT
 590
 610
 T S T A N T N M F T Y E I A P V F V L L
 TGACATCAACAGCAAACACGAACATGTTACCTATGAGGATCGCCCCCTGTATTGTA
 630
 670
 E Y V T L K K M R E I I G W P G G S G D
 TCGAATATGTGACACTAAAGAAAATGAGGGAAATCATGGCTGGCCAGGGCTCTGGCG
 710
 730
 G I F S P G G A I S N M Y A M L I A R Y
 ATGGAATCTTTCTCCTGGTGGCATCTCCAAACATGTACGGCCATGCTCATTGCCGCT
 770
 790
 K M F P E V K E K G M A A V P R L I A F
 ATAAGATGTTCCAGAAGTCAGGAAAGGGATGGCGGGTGGCCAGGCTCATCGCAT
 830
 850
 870
 T S E H S H F S L K K G A A A V P R L I A F
 TCACGGTCAAGGCTAGTCACTTTCTCAAGAAGGGAAATGTGATGAGAGGGAAAATGAT
 890
 910
 D S V I L I K C D E R G K M I P S D L E
 TCACGGTCAAGGCTAGTCTGATTAAATGTGATGAGAGGGAAAATGATCCCATCTGAC
 950
 970
 CAGACAGCGTGA
 990
 R R I L E V K Q K G F V P F L V S A T A
 AAAGAAGAATCCCTGAAAGTCAAACAGAAAGGATTGTTCCCTGGTGA
 1010
 1030
 G T T V Y G A F D P L L A V A D I C K K
 1050
 1070

Figure 2B

CTGGAAACCACTGTGTACGGGGCTTTGATCCTCTGGCTCTGGACATCTGGAA
 1090 Y K I W M H V D A A W G G G L L M S R K
 AATATAAGATCTGGATGCATGTGGATGCTGGCTTGGGGTTACTGATGTCTCGGA
 1150 H K W K L N G V E R A N S V T W N P H K
 AACACAAGTGGAAAGCTGAACGGGTGGAGGGCCAACTCTGTGACATGGAAATCCCCACA
 1210 M M G V P L Q C S A L L V R E E G L M Q
 AGATGGATGGGTGCCCCCTGCAATGTTGGCTCTGGCTCAGAGGGGACTGATGC
 1270 S C N Q M H A S Y L F Q Q D K H Y D L S
 AGAGCTGCAACCAGATGCATGCTCCTACCTCTTCAAGATAAGCACTATGACCTGT
 1330 Y D T G D K A L Q C G R H V D V F K L W
 CCTATGACACGGGAGACAAGGCCCTTGCAGTGGACGGCAACGTCCATGTCTAAATTAT
 1390 L M W R A K G T T G F E A H I D K C L E
 GGCTCATGTGGAGGAGCAAAGGGACTACTGGATTGAAGCTCACATTGATAAGTGGTTGG
 1450 L A E Y L Y N I I K N R E G Y E M V F D
 AGCTGGCAGAGTATTACAATATCATTAAAAACCGAGAAGGATATGAAATGGTGTTCG
 1510 G K P Q H T N V C F W F V P P S L R V L
 ATGGGAAGCCTCAGCACACAAATGTCGCTTCTGGTTTGTACCTCCTAGTTGGAGGTTTC
 1570 E D N E E R M S R L S K V A P V I K A R

Figure 2C

TGGAGACAATGAAGAGAATGAGCCCTCTCAAAGGTGGGCCAGTGATTAAAGCCA
 1630 1650 1670
 M M E Y G T T M V S Y Q P L G D K V N F
 GAATGGAGTATGGGACCAATGGTCAGCTACCAACCCCTTAGGAGATAAGGTCAACT
 1690 1710 1730
 F R M V I S N P A A T H Q D I D F L I E
 TCTTCCGCATGGTCATCTCAAACCCCTGCAGCAACTCACCAAGACATTGACTTCATTG
 1750 1770 1790 *~*
 E I E R L G Q D L *
 AGAAATCGAACGGCCTGGGACAAAGATTGTAATCACTTGTCAACCAAACTTTCAAGTTCT
 1810 1830 1850
 CTAGGTAGACAGCTAAGTTGTACAAACTGTGTAATGTATTGTAGTTGTTCCAGAGT
 1870 1890 1910
 ATTCTATTTCTATATCGTGGTGTACAGTAGTCCAGTTAAA
 1930 1950

Figure 2D

	M	A	S
AGCTCGCCGAGCTCGCACTCGCAGGGACCTGCTCCAGTCTCCAAAGCCGATGGCATC	10	30	50
P G S G F W S F G S E D G S G D S E N P	70	90	110
TCCGGGCTCTGGCTTTGGTCTTCGGGAAAGATGGCTCTGGGATTCGGAGAACATCC	130	150	170
CGGCACAGCGCGAGCCTGGTGCCTCAAGTGGCTCAGAAGTTCACGGGGCATCGGAAACAA	190	210	230
ACTGTGCCCTCTACGGAGACGGCCGAGAACGGCCGGAGAGCGGGAGGCCAACCC	250	270	290
P R A A R K A A C A C D Q K P C S C S	310	330	350
CCCGCGGGCCCGCCGGAAAGGCCCTGGCCTGGCAGAACAGAACGCCCCCTGCAGCTGCTC	370	390	410
K V D V N Y A F L H A T D L L P A C D G	430	450	470
CAAAGTGGATGTCAACTACGCGTTCTCCATGCAAACAGAACCTGCTGCCGTGTGATGG			
AGAAAGGCCACCTTGGCGTTCTGCAAGAGATGTTATGAACTTACTTCAGTATGTGGT			
GAAAAGTTCGATAGATCAACCAAAGTGAATTCCATTATCCTAATGAGCTTCTCCA			

Figure 3A

490 Q T T L K Y A I K T G H P R Y F N Q L S
 CCAAACAACTCTAAATATGCCAATTAAACAGGGCATCCTAGATTAATCAACTTC
 550 T G L D M V G L A A D W L T S T A N T N
 TACTGGTTGGATATGGTTGGATTAGCAGCAGACTGGCTGACATCAACAGCAAATCTAA
 610 M F T Y E I A P V F V L L E Y V T L K K
 CATGTTCACCTATGAAATTGCTCCAGTATTGCTTTGGAATATGTCACACTAAAGAA
 670 M R E I I G W P G G S G D G I F S P G G
 ATGAGAGAAATCATTGGCTGGCCAGGGGCTCTGGCGATGGATATTTCCTCCGGTGG
 730 A I S N M Y A M M I A R F K M F P E V K
 CGCCATATCTAACATGTATGCCATGATGGATCGCACCGCTTTAACATGTTCCAGAAGTCAA
 790 E K G M A A L P R L I A F T S E H S H F
 GGAGAAAGGAATGGCTGCTCTCCAGGCTCATGGCTCATGGCTTCACGTCCTGAAACATAGTCATT
 850 S L K K G A A A L G I G T D S V I L I K
 TTCTCTCAAGAAGGGAGCTGCAGCCTTAAAGGATGGAAACAGACAGCGTGTGATTCTGATTAA
 910 C D E R G K M I P S D L E R R I L E A K
 ATGTGATGAGAGGGAAAATGATTCCATCTGATCTGATTGAAAGGATTCTGAAAGCCAA
 970 Q K G F V P F L V S A T A G T T V Y G A
 510 530
 570 590
 630 650
 690 710
 750 770
 810 830
 870 890
 930 950
 990 1010

Figure 3B

ACAGAAAGGGTTTGTTCCTTCCGTGAGTGCCACAGCTGGAACCCGGTGTACGGAGC
 1030
 F D P L A V A D I C K K Y K I W M H V
 ATTTGACCCCTCTAGCTGCTGCTGACATTGCAAAAGTATAAGATCTGGATGCATGT
 1090
 D A A W G G L L M S R K H K W K L S G
 GGATGCAGCTGGGGGGATTACTGATGTCGGAAACACAAAGTGGAAACTGAGTGG
 1150
 V E R A N S V T W N P H K M M G V P L Q
 CGTGGAGGGCCAACCTCTGTGACCGTGGATTCCACACAGATGATGGGAGTCCCTTGCA
 1210
 C S A L L V R E E G L M Q N C N Q M H A
 GTGCTCTGCTCCTGGTTAGAGAAGAGGGATTGATGCAGAAATTGCAACCAAATGCATGC
 1270
 S Y L F Q Q D K H Y D L S Y D T G D K A
 CTCCTACCTCTTCAGCAAGATAAACATTATGACCCCTATGACACTGGAGACAAGGC
 1330
 L Q C G R H V D V F K L W L M W R A K G
 CTTACAGTGGGACGCCACGTTGATGTTAAACTATGGCTGATGTGGAGGGCAAAGGG
 1390
 T T G F E A H V D K C L E L A E Y L Y N
 GACTACCGGGTTGAAGCGCATGTTGATAAATGTTGGAGTTGGCAGAGTTTACAA
 1450
 I I K N R E G Y E M V F D G K P Q H T N
 CATCATAAAACCGAGAAGGATATGAGATGGTGTGATGGGAAGGCCTCAGCACACAAA
 1510
 1530
 1550

Figure 3C

V C F W Y I P P S L R T L E D N E E R M
 TGTCTGCTTCTGGTACATTCCCAAGCTTGGCTACTCTGGAAAGACAATGAAGAGAAAT
 1570
 S R L S K V A P V I K A R M M E Y G T T
 GAGTCGCCTCTCGAAGGGGGCTCCAGTGGATTAAAGCCAGAATGATGGAGATGGAAACCAC
 1630
 M V S Y Q P L G D K V N F F R M V I S N
 ATGGTCAGCTACCAACCCTGGGAGACAAGGGTCAATTCTCCGCATGGTCATCTCAA
 1690
 P A A T H Q D I D F L I E E I E R L G Q
 CCCAGGGCAACTCACCAAGACATTGACTTCCCTGATTGAAGAAATAGAACGGCTTGGACA
 1750
 1710 1730
 1770 1790
 D L *
 AGATTTATAAACCTTGCTCACCAAGCTGTTCCACTTCTTAGGTAGACAATTAAAGTTG
 1810 1830 1850
 TCACAAACTGTGAATGTATTGTAGTTGGTCCAAAGTAAATCTATTCTATATTGTC
 1870 1890 1910
 GTGTCAAAGTAGAGTTAAAAATTAAACAAAAAGACATTGCTCCTTTAAAGTCCTT
 1930 1950 1970
 CTTAAGTTAGAATAACCTCTAAGAATTCTGACAAAGGCTATGTTCTAATCAATAAG
 1990 2010 2030
 GAAAAGCTTAAATTGTTATAAACTTCCCTTACTTTAATATAAGTGTGCAAAGCAAC
 2050 2070 2090

Figure 3D

GAP WEIGHT: 3.000 LENGTH WEIGHT: 0.100 QUALITY: 856.2 RATIO: 1.464
PERCENT SIMILARITY: 97.436 4817, PEP HGT2.PEP AVERAGE MATCH: 0.540
AVERAGE MISMATCH: -0.396 LENGTH: 585 GAPS: 0 PERCENT IDENTITY: 96.068
AUGUST 22, 1990 08:20 **

1	MASPGSGFWSEFGSEDGSGDOPENPGTARAWCQVAQKFTGGIGNKLCALLYG	50
1	MASPGSGFWSEFGSEDGSGDSENPGBTARAWCQVAQKFTGGIGNKLCALLYG	50
51	DSEKPAESGGSVTSRAATRKVACTCDQKPCSCPQGDVNYYALLHHATDLLPA	100
51	DAEKPAESGGSQPPRAAARKAACACDQKPCSCSKVDVNYYAFLHHATDLLPA	100
101	CEGERPTLAFLQDVMNILLQYVVKSFDRSTKVIDFHYPNELLQEYNWELA	150
101	CDGERPTLAFLQDVMNILLQYVVKSFDRSTKVIDFHYPNELLQEYNWELA	150
151	DQPQNLEELTHCQTTLYAIKJGHPRYFNQLSTGLDMVGLAADWLSTA	200
151	DQPQNLEELIMHCQTTLYAIKJGHPRYFNQLSTGLDMVGLAADWLSTA	200
201	NTNMFTYEIAPVFVLLYVTLLKMREIIGWPGGSGDGFSPGGAIISNMYA	250
201	NTNMFTYEIAPVFVLLYVTLLKMREIIGWPGGSGDGFSPGGAIISNMYA	250

Figure 4A

251	MLIARYKMFPEVKEKGMAAVPRLLIAFTSEHSHFSLKKGAAALGIGTDSVI	300
251	MMIAREFKMFPEVKEKGMAALPRLLIAFTSEHSHFSLKKGAAALGIGTDSVI	300
301	LIKCDERGKMWIPSDLERRILEVKQKGFPFLVSATAGTVYGAFDPLLA	350
301	LIKCDERGKMWIPSDLERRILEAKQKGFPFLVSATAGTVYGAFDPLLA	350
351	ADICKKYKIWMHVDAAWGGGLLMSRKHKWKJLNGVERANSVTWNPHKMMGV	400
351	ADICKKYKIWMHVDAAWGGGLLMSRKHKWKJLSGVERANSVTWNPHKMMGV	400
401	PLQCSALLVREEGLMQSCNQMHASYLFQQDKHYDLSYDTGDKALQCCGRHV	450
401	PLQCSALLVREEGLMQNCNQMHASYLFQQDKHYDLSYDTGDKALQCCGRHV	450
451	DVFKLWLMWRAKGTTGFEAHIDKCLELAEYLINYIIKNREGYEMVFDGKPQ	500
451	DVFKLWLMWRAKGTTGFEAHVDKCLELAEYLINYIIKNREGYEMVFDGKPQ	500
501	HTNVCFWFVPPSLRVEDNEERMSRLSKVAPVIKARMMEYGTITMVSYQPL	550
501	HTNVCFWYIPPSLRTLEDNEERMSRLSKVAPVIKARMMEYGTITMVSYQPL	550
551	GDKVNFFRMVISNPAAATHQDIDFLIEEIERLQDL	585
551	GDKVNFFRMVISNPAAATHQDIDFLIEEIERLQDL	585

Figure 4B

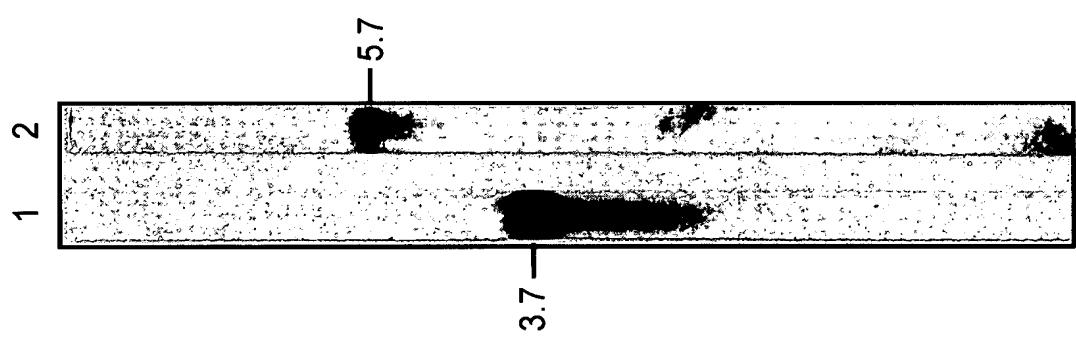


Figure 5

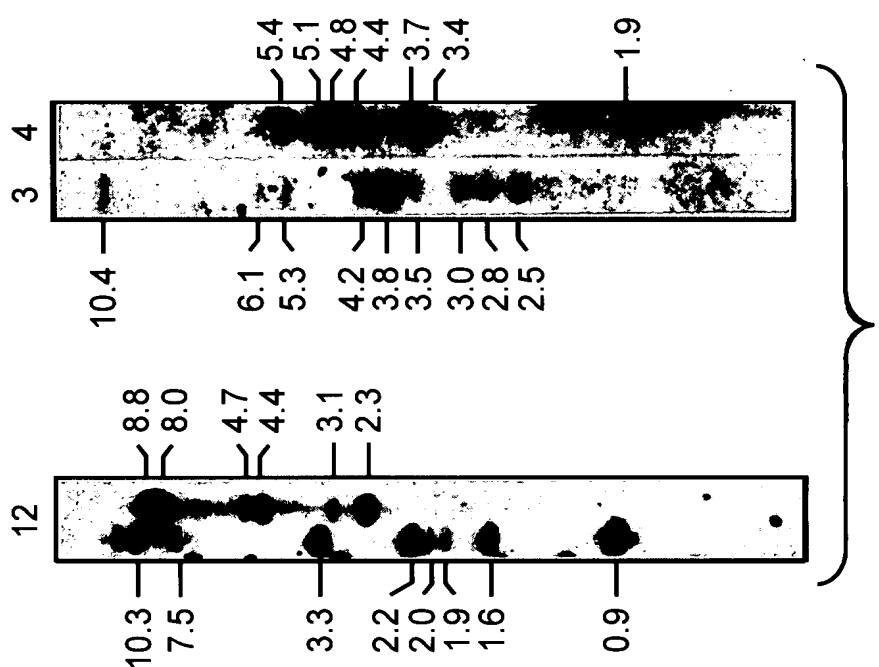


Figure 6

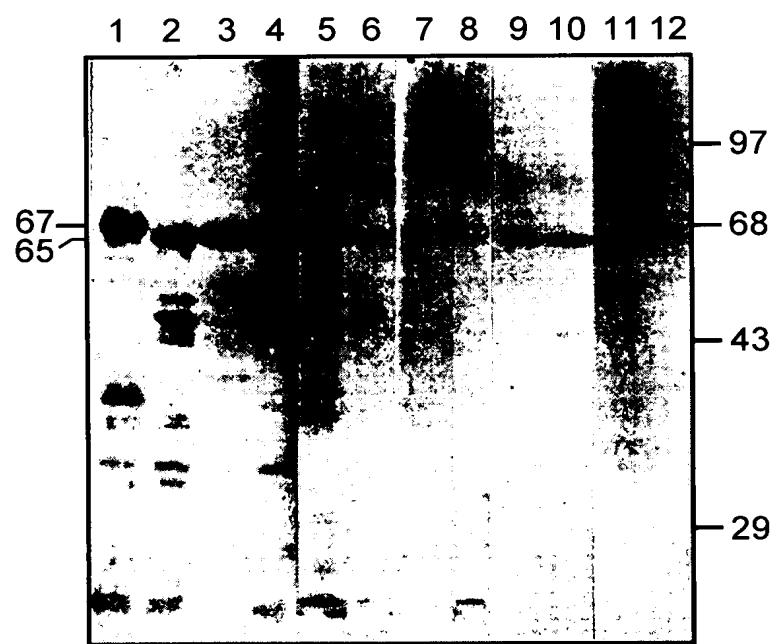


Figure 7